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**RAW SEQUENCE LISTING** DATE: 10/03/2002  
**PATENT APPLICATION:** US/09/625,573 TIME: 14:00:12

Input Set : N:\CrF3\RULE60\09625573.raw  
Output Set: N:\CRF4\10032002\I625573.raw

## **SEQUENCE LISTING**



**ENTERED**

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Input Set : N:\Crf3\RULE60\09625573.raw  
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60	(ix) FEATURE:		
62	(A) NAME/KEY: CDS		
63	(B) LOCATION: 40..1161		
65	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:		
68	GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAAC ATG CTG TCC ACA TCT	54	
69	Met Leu Ser Thr Ser		
70	1 5		
72	CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC	102	
73	Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr		
74	10 15 20		
76	ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG	150	
77	Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val		
78	25 30 35		
80	AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC	198	
81	Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe		
82	40 45 50		
84	ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC CTC ATC TTA ATA AAC	246	
85	Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn		
86	55 60 65		
88	TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC	294	
89	Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala		
90	70 75 80 85		
92	ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT	342	
93	Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser		
94	90 95 100		
96	GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA	390	
97	Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr		
98	105 110 115		
100	GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC	438	
101	Gly Leu Tyr His Ile Gly Tyr Phe Gly Ile Phe Phe Ile Ile Leu		
102	120 125 130		
104	CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA	486	
105	Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu		
106	135 140 145		
108	AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG	534	
109	Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp		
110	150 155 160 165		
112	TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC	582	
113	Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys		
114	170 175 180		
116	CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA	630	
117	Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly		
118	185 190 195		
120	TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG	678	
121	Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu		
122	200 205 210		
124	CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG	726	
125	Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu		
126	215 220 225		

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128	CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC	774
129	Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile	
130	230 235 240 245	
132	TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT	822
133	Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile	
134	250 255 260	
136	GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT	870
137	Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys	
138	265 270 275	
140	GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT	918
141	Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu	
142	280 285 290	
144	GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG	966
145	Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly	
146	295 300 305	
148	GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC	1014
149	Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala	
150	310 315 320 325	
152	CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG	1062
153	Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys	
154	330 335 340	
156	AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA	1110
157	Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly	
158	345 350 355	
160	AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA	1158
161	Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly	
162	360 365 370	
164	GCC TAGAGACAGA AATGACAGAT CTCTGCTTTG GAAATCACAC GTCTGGCTTC	1211
165	Ala	
167	ACAGATGTGT GATTACAGT GTGAATCTTG GTGTCTACGT TACCAGGCAG GAAGGCTGAG	1271
169	AGGAGAGAGA CTCCAGCTGG GTTGGAAAAC AGTATTTCC AAACCTACCTT CCAGTTCCTC	1331
171	ATTTTGAAT ACAGGCATAG AGTCAGACT TTTTTAAAT AGTAAAAATA AAATTAAAGC	1391
173	TGAAACTGC AACTTGTAAGA TGTGGTAAAG AGTTAGTTG AGTTGCTATC ATGTCAAACG	1451
175	TGAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTTG AGCTTAAGAA TTTTGAGCAG	1511
177	TGGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA	1571
179	GTGTGTGATC TGTGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT	1631
181	TGAATCACAG TATACGCTCC ATCGCTGTC A TCTCAGCTGG ATCTCCATTC TCTCAGGCTT	1691
183	GCTGCCAAAA GCCTTTGTTG TTTTGTGTTG TATCATTATG AAGTCATGCG TTTAATCACA	1751
185	TTCGAGTGT TCAGTGCTTC GCAGATGTC TTGATGCTCA TATTGTTCCC TAATTGCCA	1811
187	GTGGGAACCTC CTAAATCAAAT TTGGCTTCTA ATCAAAGCTT TAAACCCCTA TTGGTAAAGA	1871
189	ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT	1931
191	AAGAATGTTC TTATGTTGCC CAGTGTGTT CTGATCTGAT GCAAGCAAGA AACACTGGGC	1991
193	TTCTAGAACCTG AGGCAACTTG GGAACCTAGAC TCCCAAGCTG GACTATGGCT CTACTTCAG	2051
195	GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA	2111
197	TATATTTGTA TGATCTTAAT GAATGCATAA AATGTTAAGT TGATGGTGAT GAAATGTAAA	2171
199	TACTGTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA	2231
201	G	2232

204 (2) INFORMATION FOR SEQ ID NO: 2:  
206 (i) SEQUENCE CHARACTERISTICS:

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207 (A) LENGTH: 374 amino acids  
 208 (B) TYPE: amino acid  
 209 (D) TOPOLOGY: linear  
 211 (ii) MOLECULE TYPE: protein  
 213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 216 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser  
 217 1 5 10 15  
 219 Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys  
 220 20 25 30  
 222 His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu  
 223 35 40 45  
 225 Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val  
 226 50 55 60  
 228 Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr  
 229 65 70 75 80  
 231 Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro  
 232 85 90 95  
 234 Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met  
 235 100 105 110  
 237 Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile  
 238 115 120 125  
 240 Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His  
 241 130 135 140  
 243 Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr  
 244 145 150 155 160  
 246 Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile  
 247 165 170 175  
 249 Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro  
 250 180 185 190  
 252 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile  
 253 195 200 205  
 255 Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly  
 256 210 215 220  
 258 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg  
 259 225 230 235 240  
 261 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp  
 262 245 250 255  
 264 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe  
 265 260 265 270  
 267 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln  
 268 275 280 285  
 270 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile  
 271 290 295 300  
 273 Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu  
 274 305 310 315 320  
 276 Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly  
 277 325 330 335  
 279 Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp  
 280 340 345 350

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282 Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu  
283 355 360 365

285 Gln Asp Lys Glu Gly Ala  
286 370

289 (2) INFORMATION FOR SEQ ID NO: 3:

291 (i) SEQUENCE CHARACTERISTICS:

292 (A) LENGTH: 1979 base pairs  
293 (B) TYPE: nucleic acid  
294 (C) STRANDEDNESS: single  
295 (D) TOPOLOGY: linear

297 (ii) MOLECULE TYPE: cDNA  
299 (iii) HYPOTHETICAL: NO

301 (iv) ANTI-SENSE: NO

303 (ix) FEATURE:

304 (A) NAME/KEY: CDS

305 (B) LOCATION: 81..1160

307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

310	CAGGACTGCC	TGAGACAAGC	CACAAGCTGA	ACAGAGAAAG	TGGATTGAAC	AAGGACGCAT	60
312	TTCCCCAGTA	CATCCACAAC	ATG CTG TCC	ACA TCT CGT	TCT CGG	TTT ATC	110
313			Met Leu Ser	Thr Ser Arg	Ser Arg Phe	Ile	
314	1		5		10		
316	AGA AAT ACC AAC	GAG AGC GGT	GAA GAA GTC	ACC ACC TTT	TTT GAT	TAT	158
317	Arg Asn Thr Asn	Glu Ser Gly	Glu Glu Val	Thr Thr Phe	Phe Asp	Tyr	
318	15		20		25		
320	GAT TAC GGT GCT CCC	TGT CAT AAA	TTT GAC GTG	AAG CAA ATT	GGG GCC		206
321	Asp Tyr Gly Ala	Pro Cys His Lys	Phe Asp Val	Lys Gln Ile	Gly Ala		
322	30		35		40		
324	CAA CTC CTG CCT	CCG CTC TAC	TCG CTG GTG	TTC ATC TTT	GGT TTT GTG		254
325	Gln Leu Pro Pro	Leu Tyr Ser	Leu Val Phe	Ile Phe Gly	Phe Val		
326	45		50		55		
328	GGC AAC ATG CTG GTC	CTC ATC TTA ATA	AAC TGC AAA	AAG CTG AAG			302
329	Gly Asn Met Leu Val	Leu Ile Leu Ile	Asn Cys Lys	Lys Leu Lys			
330	60		65		70		
332	TGC TTG ACT GAC ATT	TAC CTG CTC AAC	CTG GCC ATC	TCT GAT CTG	CTT		350
333	Cys Leu Thr Asp Ile	Tyr Leu Leu Asn	Leu Ala Ile	Ser Asp Leu	Leu		
334	75		80		85		90
336	TTT CTT ATT ACT CTC	CCA TTG TGG GCT	CAC TCT GCT	GCA AAT GAG	TGG		398
337	Phe Leu Ile Thr Leu	Pro Leu Trp Ala	His Ser Ala	Ala Asn Glu	Trp		
338	95		100		105		
340	GTC TTT GGG AAT GCA	ATG TGC AAA TTA	TTC ACA GGG	CTG TAT CAC	ATC		446
341	Val Phe Gly Asn Ala	Met Cys Lys	Leu Phe Thr	Gly Leu Tyr	His Ile		
342	110		115		120		
344	GGT TAT TTT GGC GGA	ATC TTC ATC	CTC CTG ACA	ATC GAT AGA			494
345	Gly Tyr Phe Gly	Gly Ile Phe	Ile Leu Leu	Thr Ile Asp	Arg		
346	125		130		135		
348	TAC CTG GCT ATT	GTC CAT GCT	GTG TTT GCT	TTA AAA GCC	AGG ACG	GTC	542
349	Tyr Leu Ala Ile	Val His Ala Val	Phe Ala Leu	Lys Ala Arg	Thr Val		
350	140		145		150		
352	ACC TTT GGG GTG	GTG ACA AGT	GTG ATC ACC	TGG TTG	GTG GCT	GTG TTT	590

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09625573.raw  
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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:856 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:874 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10